

Search Result: eco:b3823 -> GENES

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```

time(seconds)      600
file(blocks)       unlimited
data(kbytes)       8340032
stack(kbytes)      8340032
memory(kbytes)     16340032
coredump(blocks)   0
nofiles(descriptors) 200
vmemory(kbytes)    16340032
concurrency(threads) 1024
FASTA searches a protein or DNA sequence data bank
version 3.4t10 Dec 12, 2001

```

Please cite:

W. R. Pearson & D. J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/WWW/get_linkdb_fasta.25159/b3823: 122 aa
>eco:b3823 yigJ; hypothetical 22.5 kD protein in recQ-pldB Intergenic region (A)
vs /bio/db/fasta/genes/genes library
searching /bio/db/fasta/genes/genes library
```

```

< 20  opt 18  0: 0:
22  0  0:
24  4  1:
26  34 15:
28  246 165:
30 1252 1005:
32 4493 3886:
34 11106 10538:
36 20359 21643:
38 31849 35767:
40 43946 49892:
42 54483 60987:
44 60488 67275:
46 63676 68521:
48 62549 65601:
50 59305 59861:
52 53651 52628:
54 46294 44953:
56 39505 37550:
58 33631 30828:
60 27692 24972:
62 23351 20020:
64 18811 15922:
66 15038 12584:
68 12020 9899:
70 9763 7757:
72 7361 6061:
74 6069 4726:
76 4755 3678:
78 3940 2859:
80 2849 2220:
82 2368 1698:
84 1810 1345:
86 1457 1041:
88 1160 805:
90 832 623:
92 743 482:
94 608 373:
96 458 289:
98 310 223:
100 265 173:
102 197 134:
104 190 104:
106 123 80:
108 102 62:

```

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110	101	48:*	:-:-:-:-
112	63	37:*	:-:-:-:-
114	44	29:*	:-:-:-:-
116	38	22:*	:-:-:-:-
118	32	17:*	:-:-:-:-
>120	398	13:*	:-:-:-:-

257957886 residues in 729837 sequences  
 statistics extrapolated from 60000 to 729458 sequences  
 Expectation\_n fit:  $\rho(\ln(x)) = 3.28164/-0.000189$ ;  $\mu = 15.2431/+0.011$   
 $\text{mean\_var} = 57.4751/+11.689$ , O's: 0 Z-trim: 3 B-trim: 3787 in 1/58  
 $\text{Lambda} = 0.1692$   
 Kolmogorov-Smirnov statistic: 0.0430 (N=29) at 50

FASTA (3.44 Dec 2001) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 36, opt: 24, open/ext: -10/-2, width: 16

Scan time: 89.390

**The best scores are:**

opt. bits E (729837)

Top 10  Clear Select operation

**Exec**

<input checked="" type="checkbox"/> <u>eca:Z5344</u>	yigJ; orf; Unknown function	( 122)	792	200	5e-51
<input checked="" type="checkbox"/> <u>ecp:b3823</u>	yigJ; hypothetical 22.5 kD protein in recQ-pldB	( 122)	792	200	5e-51
<input checked="" type="checkbox"/> <u>ecj:JW3797</u>	yigJ; Amino acid exporter (threonine)	( 155)	792	201	6.7e-51
<input checked="" type="checkbox"/> <u>ecs:ECs4753</u>	threonine efflux protein [KO:K03329]	( 206)	792	201	6.7e-51
<input checked="" type="checkbox"/> <u>sfx:S3854</u>	yigJ; hypothetical protein	( 122)	786	199	1.4e-50
<input checked="" type="checkbox"/> <u>sfl:SF3901</u>	rhtC; threonine efflux protein	( 206)	786	199	1.9e-50
<input checked="" type="checkbox"/> <u>ecc:c4745</u>	threonine efflux protein [KO:K03329]	( 206)	781	198	4.3e-50
<input checked="" type="checkbox"/> <u>xtm:STM3959</u>	rhtC; RhtB family, threonine efflux protein	( 206)	717	182	2.2e-45
<input checked="" type="checkbox"/> <u>sty:STY3600</u>	rhtC; threonine efflux protein [KO:K03329]	( 206)	717	182	2.2e-45
<input checked="" type="checkbox"/> <u>stt:t3338</u>	rhtC; threonine efflux protein [KO:K03329]	( 206)	717	182	2.2e-45
<input type="checkbox"/> <u>eca:ECA4171</u>	rhtC; threonine efflux protein	( 207)	561	144	6.3e-34
<input type="checkbox"/> <u>ypm:YP3216</u>	rhtC; threonine efflux protein	( 206)	560	144	7.5e-34
<input type="checkbox"/> <u>ypk:y0398</u>	threonine efflux protein	( 206)	560	144	7.5e-34
<input type="checkbox"/> <u>xpe:YPO3832</u>	rhtC; threonine efflux protein	( 206)	560	144	7.5e-34
<input type="checkbox"/> <u>pmu:PMO727</u>	hypothetical H11307	( 214)	240	86	2.5e-10
<input type="checkbox"/> <u>bha:BH2932</u>	unknown conserved protein	( 210)	229	63	1.6e-09
<input type="checkbox"/> <u>pst:PSPT02958</u>	rhtC; threonine efflux protein	( 214)	227	63	2.2e-09
<input type="checkbox"/> <u>bms:BR1920</u>	transporter, LysE family	( 212)	221	61	6.1e-09
<input type="checkbox"/> <u>bme:BME10143</u>	threonine efflux protein	( 212)	221	61	6.1e-09
<input type="checkbox"/> <u>hin:H11307</u>	hypothetical protein H11307 [KO:K03329]	( 210)	220	61	7.2e-09
<input type="checkbox"/> <u>pst:PSPT01147</u>	transporter, LysE family	( 210)	216	60	1.4e-08
<input type="checkbox"/> <u>cdi:DIP1767</u>	putative LysE type translocator	( 212)	216	60	1.4e-08
<input type="checkbox"/> <u>sme:SMc02484</u>	putative amino acid efflux transmembrane prot	( 214)	210	59	4e-08
<input type="checkbox"/> <u>ppr:PBPR3511</u>	hypothetical threonine efflux protein	( 218)	210	59	4e-08
<input type="checkbox"/> <u>vch:VC0191</u>	conserved hypothetical protein	( 222)	206	58	7.9e-08
<input type="checkbox"/> <u>atu:Atu2633</u>	rhtB; RhtB family transporter	( 204)	201	57	1.8e-07
<input type="checkbox"/> <u>atc:AGR_C_4773</u>	amino acid efflux-like protein	( 216)	201	57	1.8e-07
<input type="checkbox"/> <u>ecs:c0448</u>	yahN; resistance factor to homoserine/threonine.	( 224)	201	57	1.9e-07
<input type="checkbox"/> <u>aji:JW0220</u>	yahN; resistance factor to homoserine/threonine	( 223)	198	56	3.1e-07
<input type="checkbox"/> <u>eco:b0328</u>	yahN; putative cytochrome subunit of dehydrogena	( 223)	198	56	3.1e-07
<input type="checkbox"/> <u>ece:Z0424</u>	yahN; putative cytochrome subunit of dehydrogena	( 223)	198	56	3.1e-07
<input type="checkbox"/> <u>ecs:ECs0382</u>	putative cytochrome subunit of dehydrogenase [	( 223)	198	56	3.1e-07
<input type="checkbox"/> <u>cgl:NCg10143</u>	Cgl10148; putative threonine efflux protein	( 226)	197	56	3.7e-07
<input type="checkbox"/> <u>stm:STM0365</u>	yahN; paral putative transport protein [KO:K03	( 210)	194	55	5.9e-07
<input type="checkbox"/> <u>sty:STY0397</u>	RhtC-like transporter	( 210)	194	55	5.9e-07

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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<input type="checkbox"/> aci:ACIAD3166	putative amino-acid efflux transmembrane pro	( 211)	150	44	0.001
<input type="checkbox"/> son:SO0530	transoorter, LysE family	( 203)	149	44	0.0012
<input type="checkbox"/> mla:mlr3188	hypothetical protein	( 204)	149	44	0.0012
<input type="checkbox"/> bce:BC2291	transporter, LysE family	( 210)	149	44	0.0012
<input type="checkbox"/> apr:PPRA2833	putative threonine efflux protein	( 217)	149	44	0.0012
<input type="checkbox"/> dnu:DVU0969	efflux protein, LysE family	( 248)	148	44	0.0015
<input type="checkbox"/> bpa:BP4358	putative membrane protein	( 208)	147	43	0.0017
<input type="checkbox"/> aci:JH1787	yeaS; Hypothetical protein	( 212)	147	43	0.0017
<input type="checkbox"/> eco:b1798	yeaS; hypothetical 23.2 kD protein in gapA-rnd i	( 212)	147	43	0.0017
<input type="checkbox"/> prr:PPRB1092	conserved hypothetical protein	( 214)	147	43	0.0017
<input type="checkbox"/> cvi:CV1453	conserved hypothetical protein	( 203)	146	43	0.0019
<input type="checkbox"/> ecs:ECs2507	hypothetical protein	( 212)	146	43	0.002
<input type="checkbox"/> pae:PA2710	hypothetical protein	( 204)	145	43	0.0023
<input type="checkbox"/> bpa:BP3532	putative membrane protein	( 202)	143	42	0.0032
<input type="checkbox"/> btk:BT9727_1730	transporter, LysE family	( 208)	143	42	0.0033
<input type="checkbox"/> bbr:BB4942	putative membrane protein	( 248)	143	42	0.0036
<input type="checkbox"/> ppv:PP1248	transporter, LysE family	( 255)	143	43	0.0036
<input type="checkbox"/> ecc:c2205	yeaS; hypothetical protein yeaS	( 212)	142	42	0.0039
<input type="checkbox"/> ych:VC1421	conserved hypothetical protein	( 212)	141	42	0.0046
<input type="checkbox"/> ppv:PP3625	transporter, LysE family	( 213)	141	42	0.0046
<input type="checkbox"/> sme:SMc03887	putative amino acid efflux protein	( 215)	141	42	0.0047
<input type="checkbox"/> voa:VP1379	putative homoserine/homoserine lactone efflux p	( 219)	141	42	0.0047
<input type="checkbox"/> baa:BA_2849	lysE; LysE type translocator	( 210)	140	42	0.0054
<input type="checkbox"/> pae:PA1620	hypothetical protein	( 213)	139	41	0.0065
<input type="checkbox"/> cvi:CV0188	probable homoserine/homoserine lactone efflux p	( 209)	138	41	0.0076
<input type="checkbox"/> prr:PP3565	transporter, LysE family	( 203)	137	41	0.0089
<input type="checkbox"/> rra:RPA0900	probable Rht family transporter, amino acid ef	( 210)	137	41	0.009
<input type="checkbox"/> cvi:CV2046	conserved hypothetical protein	( 211)	137	41	0.0091
<input type="checkbox"/> cvi:CV3803	conserved hypothetical protein	( 216)	137	41	0.0092
<input type="checkbox"/> ece:Z2841	yeaS; orf, hypothetical protein	( 212)	136	41	0.011
<input type="checkbox"/> aci:ACIAD2743	putative amino acid efflux transmembrane pro	( 213)	136	41	0.011
<input type="checkbox"/> bpa:BP1447	LysE-family efflux protein	( 214)	136	41	0.011
<input type="checkbox"/> bbc:BB2521	LysE-family efflux protein	( 214)	138	41	0.011
<input type="checkbox"/> sma:SAV3361	hypothetical protein	( 217)	136	41	0.011
<input type="checkbox"/> bar:GBAA1890	homoserine/threonine efflux protein, putative	( 208)	135	40	0.013
<input type="checkbox"/> baa:BA_2392	lysE; LysE type translocator	( 208)	135	40	0.013
<input type="checkbox"/> bat:BAS1752	homoserine/threonine efflux protein, putative	( 208)	135	40	0.013
<input type="checkbox"/> ban:BA1890	homoserine/threonine efflux protein, putative	( 208)	135	40	0.013
<input type="checkbox"/> prr:PP381131	putative transporter protein	( 204)	134	40	0.015
<input type="checkbox"/> mma:MM3123	hypothetical protein	( 211)	134	40	0.015
<input type="checkbox"/> bja:bj15451	rht8; RhtB family transporter	( 208)	133	40	0.018
<input type="checkbox"/> vvx:VY1593	putative threonine efflux protein	( 211)	133	40	0.018
<input type="checkbox"/> vvu:VV12697	putative threonine efflux protein	( 211)	133	40	0.018
<input type="checkbox"/> bpe:BP0568	putative amino acid efflux protein	( 209)	132	40	0.021
<input type="checkbox"/> bja:bj17736	putative efflux protein	( 210)	132	40	0.021
<input type="checkbox"/> rra:RPA1283	homoserine/homoserine lactone/threonine efflux	( 205)	131	39	0.025
<input type="checkbox"/> ppv:PP0699	transporter, LysE family	( 204)	130	39	0.029
<input type="checkbox"/> cvi:CV2839	probable transporter transmembrane protein	( 205)	130	39	0.029

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<input type="checkbox"/> pto:pt14618	hypothetical protein	( 205)	114	35	0.44
<input type="checkbox"/> vpa:VPA1206	conserved hypothetical protein	( 208)	114	35	0.44
<input type="checkbox"/> gsu:GSU1194	transporter, LysE family	( 206)	114	35	0.44
<input type="checkbox"/> vvy:VVA1119	putative threonine efflux protein	( 210)	114	35	0.44
<input type="checkbox"/> vvu:VV20571	putative threonine efflux protein	( 210)	114	35	0.44
<input type="checkbox"/> ypa:VPA0532	conserved hypothetical protein	( 210)	114	35	0.44
<input type="checkbox"/> sme:SMc02981	putative amino acid efflux transmembrane prot	( 211)	113	35	0.53
<input type="checkbox"/> cef:CE1357	lysE; lysine exporter protein	( 235)	113	35	0.56
<input type="checkbox"/> vvu:VV20771	putative threonine efflux protein	( 187)	112	35	0.58
<input type="checkbox"/> aci:ACIAD0173	rhtB; homoserine/homoserine lactone efflux p	( 208)	112	35	0.62
<input type="checkbox"/> bha:BH3495	dihydrodipicolinate reductase	( 208)	112	35	0.62
<input type="checkbox"/> atu:Atu3460	rhtB; RhtB family transporter	( 210)	112	35	0.62
<input type="checkbox"/> pst:PSPT01885	efflux protein, LysE family	( 213)	112	35	0.63
<input type="checkbox"/> yvy:VVA1297	putative threonine efflux protein	( 215)	112	35	0.63
<input type="checkbox"/> sme:SMc00542	hypothetical transmembrane protein	( 296)	113	35	0.63
<input type="checkbox"/> vpa:VPA1232	conserved hypothetical protein	( 204)	111	35	0.72
<input type="checkbox"/> atc:AGR_L_2738	conserved hypothetical protein	( 278)	112	35	0.73
<input type="checkbox"/> pae:PA5341	hypothetical protein	( 206)	111	35	0.73
<input type="checkbox"/> cyl:CV4042	probable amino acid efflux protein	( 209)	111	35	0.73
<input type="checkbox"/> sme:SMc03827	putative amino acid efflux transmembrane prot	( 213)	111	35	0.74
<input type="checkbox"/> oih:OIO964	hypothetical conserved protein	( 171)	109	34	0.92

>>eco:25344 ylgJ; orf; Unknown function (122 aa)  
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E0: 5e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

```

      10      20      30      40      50      60      70
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
eco:25 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
      10      20      30      40      50      60      70

      80      90     100     110     120
eco:b3 LIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
      :
eco:25 LIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
      :
      80      90     100     110     120

```

>>eco:b3823 ylgJ; hypothetical 22.6 kD protein in recQ-pldB inter (122 aa)  
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E0: 5e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

```

      10      20      30      40      50      60      70
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
eco:b3 MGQQLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFA
      :
      10      20      30      40      50      60      70

      80      90     100     110     120
eco:b3 LIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
      :
eco:b3 LIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
      :
      80      90     100     110     120

```

>>ecj:JW3797 ylgJ; Amino acid exporter (threonine) (155 aa)  
 initn: 799 initl: 799 opt: 792 Z-score: 1052.7 bits: 200.6 E0: 5.7e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:34-155)

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLT
          .....
ecj:JW LGWDCAAWPAFDYRKNGLAAYADYGGRWLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLT
          10      20      30      40      50      60      70

          40      50      60      70      80      90      100
eco:b3 NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDGFA
          .....
ecj:JW NLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDGFA
          80      90      100      110      120      130      140

          110      120
eco:b3 GALFAGFGIHLIISR
          .....
ecj:JW GALFAGFGIHLIISR
          150
  
```

>>ecs:ECs4753 threonine efflux protein [KO:K03329] (206 aa)  
 initn: 799 initl: 799 opt: 792 Z-score: 1051.5 bits: 200.8 E0: 6.7e-51  
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:85-206)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          .....
ecs:EC MWAGIALLGLHLII EKMAWLHTLI MVGGGLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          50      60      70      80      90      100      110

          40      50      60      70      80      90      100
eco:b3 LTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDG
          .....
ecs:EC LTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDG
          120      130      140      150      160      170      180

          110      120
eco:b3 FAGALFAGFGIHLIISR
          .....
ecs:EC FAGALFAGFGIHLIISR
          190      200
  
```

>>sfx:S3854 yigJ: hypothetical protein (122 aa)  
 initn: 786 initl: 786 opt: 786 Z-score: 1045.9 bits: 199.0 E0: 1.4e-50  
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:1-122)

```

          10      20      30      40      50      60      70
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFA
          .....
sfx:S3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTTARWGIFA
          10      20      30      40      50      60      70

          80      90      100      110      120
eco:b3 LIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          .....
sfx:S3 LIIVETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR
          80      90      100      110      120
  
```

>>sfl:SF3901 rhtC; threonine efflux protein (206 aa)  
 initn: 793 initl: 793 opt: 786 Z-score: 1043.6 bits: 199.3 E0: 1.9e-50  
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:85-206)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          .....
sfl:SF MWAGIALLGLHLII EKMAWLHTLI MVGGGLYLCW MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
          50      60      70      80      90      100      110
  
```

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40 60 80 100  
eco:b3 LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
sfl:SF LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
120 130 140 150 160 170 180

110 120  
eco:b3 FAGALFAGFGIHLIISR  
sfl:SF FAGALFAGFGIHLIISR  
190 200

>>eco:c4745 threonine efflux protein [KO:K03329] (206 aa)  
initn: 788 initl: 788 opt: 781 Z-score: 1037.0 bits: 198.1 E0: 4.3e-50  
Smith-Waterman score: 781: 98.361% identity (98.361% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
ecc:c4 MVWAGIALLGLHLIEKMAWLHTIIMVGGGLYLCWAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
50 60 70 80 90 100 110

40 60 80 100  
eco:b3 LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
ecc:c4 LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
120 130 140 150 160 170 180

110 120  
eco:b3 FAGALFAGFGIHLIISR  
ecc:c4 FAGALFAGFGIHLIISR  
190 200

>>stm:STM3959 rhtC; RhtB family, threonine efflux protein (206 aa)  
initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E0: 2.2e-45  
Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
stm:ST MVWAGIALLGLHLIEKMAWLHTIIMVGGGLYLCWAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
50 60 70 80 90 100 110

40 60 80 100  
eco:b3 LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
stm:ST LTNLANPKAIYFGSVFSLFVGDNVGTTARWGFALIIIVETLAWFTVVASLFALPQMRGQRLAKWIDG  
120 130 140 150 160 170 180

110 120  
eco:b3 FAGALFAGFGIHLIISR  
stm:ST FAGALFAGFGIHLIISR  
190 200

>>sty:STY3600 rhtC; threonine efflux protein [KO:K03329] (206 aa)  
initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E0: 2.2e-45  
Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30  
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL  
sty:ST MVWAGIALLGLHLIEKMAWLHTIIMVGGGLYLCWAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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```

      50      60      70      80      90      100      110
      40      50      60      70      80      90      100
eco:b3 LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIVETLAWFTTVVASLFALPQMRGQRLAKWIDG
      .....
sty:ST LTNLSNPKAIIYFGSVFSLFVGDNVGAARWGIFALITLETLAWFTTVVASLFALPQMRGQRLAKWIDG
      120      130      140      150      160      170      180

      110      120
eco:b3 FAGALFAGFGIHLIISR
      .....
sty:ST FAGALFAGFGIHLIISR
      190      200
```

>>stt:t3338 rhtC: threonine efflux protein [KO:K03329] (206 aa)  
initn: 724 initl: 724 opt: 717 Z-score: 852.6 bits: 182.5 E0: 2.2e-45  
Smith-Waterman score: 717; 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

```

      10      20      30
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
      .....
stt:t3 MVWAGVALLGLHLIEKMAWLHTIIMVGGGLYLCWAGYQMLRGALKKQDAASSPHIELAQSGRSFLKGL
      50      60      70      80      90      100      110

      40      50      60      70      80      90      100
eco:b3 LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIVETLAWFTTVVASLFALPQMRGQRLAKWIDG
      .....
stt:t3 LTNLSNPKAIIYFGSVFSLFVGDNVGAARWGIFALITLETLAWFTTVVASLFALPQMRGQRLAKWIDG
      120      130      140      150      160      170      180

      110      120
eco:b3 FAGALFAGFGIHLIISR
      .....
stt:t3 FAGALFAGFGIHLIISR
      190      200
```

>>eca:ECA4171 rhtC: threonine efflux protein (207 aa)  
initn: 577 initl: 533 opt: 561 Z-score: 746.8 bits: 144.4 E0: 6.3e-34  
Smith-Waterman score: 561; 66.667% identity (67.213% ungapped) in 123 aa overlap (1-122:85-207)

```

      10      20      30
eco:b3 MGYQMLRGALKKEAV-SAPAPQVELAKSGRSFLKG
      .....
eca:EC VVWAAIALGLHLLQKMAWLHTAIVGGGLYLCWAGYQMLRSARSKAQLETTQETAVVLPQRGKTFMRG
      50      60      70      80      90      100      110

      40      50      60      70      80      90      100
eco:b3 LLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIVETLAWFTTVVASLFALPQMRGQRLAKWIDG
      .....
eca:EC LLTNLANPKAIIYFGSVFSLFVGDSVSGARWGLFALISIEILLWFSLVAVFALPTMRRGQRLAKWVD
      120      130      140      150      160      170      180

      110      120
eco:b3 GFAGALFAGFGIHLIISR
      .....
eca:EC GVAGVLTGFGIHLIFSR
      190      200
```

>>ypm:YP3216 rhtC: threonine efflux protein (206 aa)  
initn: 567 initl: 567 opt: 560 Z-score: 745.5 bits: 144.1 E0: 7.5e-34  
Smith-Waterman score: 560; 67.213% identity (67.213% ungapped) in 122 aa overlap (1-122:85-206)

```

      10      20      30
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
      .....

```

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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```

eco:b3          MGYQMLR-CALKKEAVSAPAPQVELAKSG-RSFL
bms:BR MMHVITYTVLGLGLIISRSIYLFNIVKWCYVAYLVYIGFKALRAGTTKIEA-GPDLKEPRRKQGFKAAG
      60      70      80      90      100      110      120

      40      50      60      70      80      90      100
eco:b3 KGLLTNLNPKAIYFGSVFSLFVGDNVGTARWGI FALIVETLAWFTVVASLFALPQMRGQYQLAKW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bms:BR LGFAANALNPKAVFFFLSIFSTVVHVHTPTEVKLGYGVMATALISWFGVVSFFMTTPKMRRAAFSRASKW
      130      140      150      160      170      180      190

      110      120
eco:b3 IDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bms:BR IDRTSGVVFIALGLKATEKAM
      200      210
  
```

>>bme:BME10143 threonine efflux protein (212 aa)  
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E0: 6.1e-09  
Smith-Waterman score: 221; 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

```

eco:b3          10      20      30
                MGYQMLR-CALKKEAVSAPAPQVELAKSG-RSFL
bme:BM MMHVITYTVLGLGLIISRSIYLFNIVKWCYVAYLVYIGFKALRAGTTKIEA-GPDLKEPRRKQGFKAAG
      60      70      80      90      100      110      120

      40      50      60      70      80      90      100
eco:b3 KGLLTNLNPKAIYFGSVFSLFVGDNVGTARWGI FALIVETLAWFTVVASLFALPQMRGQYQLAKW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bme:BM LGFAANALNPKAVFFFLSIFSTVVHVHTPTEVKLGYGVMATALISWFGVVSFFMTTPKMRRAAFSRASKW
      130      140      150      160      170      180      190

      110      120
eco:b3 IDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
bme:BM IDRTSGVVFIALGLKATEKAM
      200      210
  
```

>>hin:HI1307 hypothetical protein HI1307 [KO:K03329] (210 aa)  
initn: 203 initl: 203 opt: 220 Z-score: 296.9 bits: 61.2 E0: 7.2e-09  
Smith-Waterman score: 220; 36.000% identity (39.474% ungapped) in 125 aa overlap (1-119:82-201)

```

eco:b3          10      20      30
                MGYQMLRGALKKEAVSAPAPQVELAKSG-RSFL
hin:HI AFWGMLSMLGLAVLFVTIPALHGVIMLLGGSYLAYLGLFMARS-KKYAKFESHSDTEFNQQTIIKKEIL
      50      60      70      80      90      100      110

      40      50      60      70      80      90
eco:b3 KGLLTNLNPKAIYFGSVFSLFVGDNVGTARWGI FALIVETLAWFTVVASLFALPQMRGQYQL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
hin:HI KGLLVNLSNAKVVVYFSSVMSLVL-VNITEMHQIILAFAVVVFETFCYFYISLIFSRNIAKRLYSQY
      120      130      140      150      160      170      180

      100      110      120
eco:b3 AKWIDGFAGALFAGFGIHLIISR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
hin:HI SRYIDNMAGIVFLFFGCVLVYNGINEIHH
      190      200      210
  
```

>>pst:PSPT01147 transporter, LysE family (210 aa)  
initn: 213 initl: 213 opt: 216 Z-score: 291.7 bits: 60.2 E0: 1.4e-08  
Smith-Waterman score: 216; 28.689% identity (28.926% ungapped) in 122 aa overlap (1-121:86-207)

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta\\_25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta_25159/result_genes.html)

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```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNL
          40      50      60      70      80      90     100     110     120     130
ppr:PB LLIHQQPTLFALLQAAGGLYLLWLGIGAVRSVLMPIFRPTAHTETVTAP---QRIIANRKQALVKGFTTN
          70      80      90     100     110     120     130

          40      50      60      70      80      90     100
eco:b3 ANPKAIIYFGSVFSLFVGDNVGTARWGI FALII VETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGA
          110      120
ppr:PB LNPKALVFFISLLSTIVPDMSTSGKITAIAILWITSFLWFAMLAWLITGKRLQOKIQWTPYIDGICGV
          140     150     160     170     180     190     200

          110      120
eco:b3 LFAGFG---IHLIISR
          130
ppr:PB LFTVIGSMILLNLLVAR
          210

```

>>vch:VCD191 conserved hypothetical protein (222 aa)  
 initn: 191 initl: 191 opt: 206 Z-score: 278.2 bits: 57.8 E0: 7.9e-08  
 Smith-Waterman score: 206; 27.826% Identity (29.091% ungapped) in 115 aa overlap (1-111:87-200)

```

          10      20      30
eco:b3      NGYQMLRGALKKEAVS---APAPQVELAKSGRSF
          40      50      60      70      80      90     100     110     120
vch:VC LVHLILSLSGISYLVKQPMFLFNLLQLAGGSYLLYLGAQLQSVMAQKNASTPTHSAPPSI-LGNRRQAF
          60      70      80      90     100     110     120

          40      50      60      70      80      90     100
eco:b3 LKGLLTNLNPKAIIYFGSVFSLFVGDNVGTARWGI FALII VETLAWFTVVASLFALPQMRRGYQRLAK
          110      120
vch:VC TKGMNTNLLNPKALVFFVSLSSLI PASMSVSGKVSAAAILVGLSLTWFSCLAWLTTSAHQQRMRITR
          130     140     150     160     170     180     190

          110      120
eco:b3 WIDGFAGALFAGFGIHLIISR
          130
vch:VC SVDSICAAVFILAGGVILWQASRAIAQTFGWL
          200     210     220

```

>>atu:Atu2633 rhtB; RhtB family transporter (204 aa)  
 initn: 200 initl: 200 opt: 201 Z-score: 272.0 bits: 56.5 E0: 1.8e-07  
 Smith-Waterman score: 201; 33.065% Identity (35.345% ungapped) in 124 aa overlap (1-118:77-198)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-
          40      50      60      70      80      90     100     110
atu:At MFHVTTYTLGLGLIISQSIYLFNIVKWLGVAYLIYIGIKALR-AGKTELPTAEGGEDVRAKSDQTGLKA
          50      60      70      80      90     100     110

          40      50      60      70      80      90
eco:b3 ---GLLTNLNPKAIIYFGSVFSLFVGDNVGTARWGI FALII VETLA-WFTVVASLFALPQMRRGYQRL
          110      120
atu:At FTLGFAANALNPKPVFFFLSIFSTVVHAHTPVGKIFG-YGLVMASCLILWFVGVSLFMTTPRMRAAFQRA
          120     130     140     150     160     170

          100      110      120
eco:b3 AKWIDGFAGALFAGFGIHLIISR
          130
atu:At SQWIDRTSGVVFIALGIKLATEKAA
          180     190     200

```

>>atc:AGR\_C.4773 amino acid efflux-like protein (216 aa)  
 initn: 200 initl: 200 opt: 201 Z-score: 271.8 bits: 56.6 E0: 1.8e-07

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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Smith-Waterman score: 201; 33.065% identity (35.345% ungapped) in 124 aa overlap (1-118:89-210)

```

          10      20      30
eco:b3      MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-
          40      50      60      70      80      90      100      110      120
atc:AG MFHVTYITLGLGLIISQSIYLFNIVKVLGVAYLIYIGIKALR-AGKTELPTAEGGEDGVRAKSDQTGLKA
          60      70      80      90      100      110      120

          40      50      60      70      80      90
eco:b3  ---GLLTNLANPKAIYFGSVFSLFVGDNVGTTARWGI FALIIVETLA-WFTVVASLFALPQMRGQRL
          100      110      120      130      140      150      160      170      180      190
atc:AG FTLGFAANALNPKPVFFLSIFSTVVAHTPVGKFG-YGLVMASCLILWFVGVSLFMTTPKRAAFQRA
          130      140      150      160      170      180      190

          100      110      120
eco:b3  AKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180      190
atc:AG SQWIDRTSGVVFALGKILATEKAA
          200      210

```

>>eco:c0448 yahN; resistance factor to homoserine/threonine. RhtB (224 aa)  
initn: 204 initl: 204 opt: 201 Z-score: 271.6 bits: 56.6 E0: 1.9e-07  
Smith-Waterman score: 201; 34.783% identity (37.209% ungapped) in 92 aa overlap (31-119:129-217)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
ecc:c0      GAYLLWFAWCSSMRHSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLHAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3      WGI FALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180      190      200      210      220
ecc:c0      LMAWAGIVLASIWRVFLSQAFSLPAVRRAYGRNQRVASWV---ICAIIGVFALRLIYEGVTQR
          170      180      190      200      210      220

```

>>ecj:JW0320 yahN; resistance factor to homoserine/threonine. Rht (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07  
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
ecj:JW      GGAYLLWFAWCSSMRQSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3      WGI FALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180      190      200      210      220
ecj:JW      LMAWAGIVLASIWRVFLSQAFSLPAVRRAYGRNQRVASRVICAIIGVFALRLIYEGVTQR
          170      180      190      200      210      220

```

>>eco:b0328 yahN; putative cytochrome subunit of dehydrogenase [K (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07  
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

```

          10      20      30      40      50      60
eco:b3      MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTTAR
          70      80      90      100      110      120
eco:b0      GGAYLLWFAWCSSMRQSTPQMSTLQQPI SAPWYVFFRRGLITDLSNPQTVLFFISIFSVTLNAETPTWAR
          130      140      150      160

          70      80      90      100      110      120
eco:b3      WGI FALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR
          130      140      150      160      170      180      190      200      210      220

```

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta\\_25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta_25159/result_genes.html)

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eco:b0 LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR  
170 180 190 200 210 220

>>ece:Z0424 yahN: putative cytochrome subunit of dehydrogenase OK (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07  
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR  
10 20 30 40 50 60  
ece:Z0 GGAYLLWFAWCSMRQSTPQNSTLQQPINAPWYVFFRRGLITLSNPQTVLFFISIFSVTLNAETPTWAR  
100 110 120 130 140 150 160

eco:b3 WGIFALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR  
70 80 90 100 110 120  
ece:Z0 LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR  
170 180 190 200 210 220

>>ecs:ECs0382 putative cytochrome subunit of dehydrogenase (KO:K0 (223 aa)  
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07  
Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR  
10 20 30 40 50 60  
ecs:EC GGAYLLWFAWCSMRQSTPQNSTLQQPINAPWYVFFRRGLITLSNPQTVLFFISIFSVTLNAETPTWAR  
100 110 120 130 140 150 160

eco:b3 WGIFALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALFAGFGIHLIISR  
70 80 90 100 110 120  
ecs:EC LMAWAGIVLASIIWRVFLSQAFSLPAVRRAYGRMQRVASRVIGAIIGVFALRLIYEGVTQR  
170 180 190 200 210 220

>>cgl:NCg10143 Cg10146: putative threonine efflux protein (226 aa)  
initn: 138 initl: 138 opt: 197 Z-score: 266.3 bits: 55.6 E0: 3.7e-07  
Smith-Waterman score: 197; 35.398% identity (38.482% ungapped) in 113 aa overlap (9-119:108-213)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR  
10 20 30 40  
cgl:NC LLQLVGGGYLTWYGIGAVRSWWTKRSTQQAADSQAVENTLVATAASGVWPAIRS—GIATNLSNPK  
80 90 100 110 120 130

eco:b3 AIIYFGSVFSLFVGDNVGTARWGIF—ALIIVETLAWFTVVASLFALPQMRGQRLAKWIDGFAGALF  
50 60 70 80 90 100 110  
cgl:NC AVLFFGSVFAQFVRPDWGIG—WSIFIGVFLTLTGLLWFGFAVL—VRKLAAGLTRNGAIIIDLTGVIF  
140 150 160 170 180 190 200

eco:b3 AGFGIHLIISR  
120  
cgl:NC IGLGMPMIFEGVVGIGGRVVG  
210 220

>>stm:STM0365 yahN: paral putative transport protein (KO:K03329) (210 aa)  
initn: 202 initl: 202 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07  
Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAR  
10 20 30 40 50 60  
stm:ST GGAYLLWFAWNSIRHQATPQNSTLQTPIAAPWTIFFRRGLMTLSNPQTVLFFISIFSVTLNAETPTWAR  
100 110 120 130 140 150 160

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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ZUU4 09/00 月 19:39 AAA 筑仙付武寺研所

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```

          90      100      110      120      130      140      150
          60      70      80      90      100      110      120
eco:b3 LFVGDNVGTTARWGIF--ALIIVETLAWFTVVASLFAIPQMRRGYQRLAKWIDGFAGALFAGFGIHLIIS
cef:CE QFITPDGCVG--WSIFLAVFLILYGLVWFLGFAVLVRSFAAR--ITRNAVIDLFTGVIFIALGFMVWVQ
          160      170      180      190      200      210      220

```

eco:b3 R

cef:CE GVVGIGSWILG  
230

>>eca:ECA3867 putative LysE-type translocator (204 aa)  
initn: 180 initl: 180 opt: 190 Z-score: 257.5 bits: 53.8 E0: 1.1e-06  
Smith-Waterman score: 190; 30.645% identity (33.043% ungapped) in 124 aa overlap (1-120:85-203)

```

                                10      20      30
                                MGYQNL--RGALKKEAVSAPAPQVELAKSGRSFLK
eca:EC ATHMAYCVAGLAVVITTPWLFNVLKYAGAAYLIWIGIQALFTRGSGMDVSNLTQQSVSLKKA--FLQ
          50      60      70      80      90      100      110

```

```

          40      50      60      70      80      90      100
eco:b3 GLLTNLNLPKAIIVFGSVFSLFVGDNVGTTAR--WGIFALII-VETLAWFTVVASLFAIPQMRRGYQRLAK
          120      130      140      150      160      170      180
eca:EC GYLCNLLNPKATLFFLAMFTQVLNIHSGIGEKLV--YAMIIWLLSLVWVPLLVVLFQSEPVRRLAKVQK
          120      130      140      150      160      170      180

```

```

          110      120
eco:b3 WIDGFAGALFAGFGIHLIISR
          190      200
eca:EC LVOKLLGTVLIALGKVALG
          190      200

```

>>pae:PA4507 hypothetical protein (210 aa)  
initn: 197 initl: 116 opt: 182 Z-score: 246.8 bits: 51.9 E0: 4.5e-06  
Smith-Waterman score: 182; 35.294% identity (42.857% ungapped) in 136 aa overlap (1-122:83-208)

```

                                10      20      30
                                MGYQMLRG--ALK-KEAVSAPA-PQVELAKSGRS
pae:PA ACHYLMAATGLALLFRTAPWTFDLVRLGAVYLANLGLQMLRGGLALPTSDAGSAPVVPHADR--RA
          50      60      70      80      90      100      110

```

```

          40      50      60      70      80      90
eco:b3 FLKGLLTNLNLPKAIIVFGSVFSLFVGDNVGTTA--RWGIFALII-VETLAWFTVVASLFAIPQMRRGY--
          120      130      140      150      160      170      180
pae:PA LLRGLLTNLNLPKALLFCSVLLPQFVSPEAGSLAVQFAALGTVLVVLGLAFDCA--YALAGGRLGRWLA
          120      130      140      150      160      170      180

```

```

          100      110      120
eco:b3 ---QRLAKWIDGFAGALFAGFGIHLIISR
          190      200      210
pae:PA SRPRAQRLQW--GFCG-LLIGCYRLALLRQL
          190      200      210

```

>>cvi:CV3240 rhtC; Threonine efflux protein (207 aa)  
initn: 171 initl: 171 opt: 181 Z-score: 245.6 bits: 51.6 E0: 5.2e-06  
Smith-Waterman score: 181; 25.620% identity (25.833% ungapped) in 121 aa overlap (1-120:86-206)

```

          10      20      30
          MGYQMLRGALKK--EAVSAPAPQVELAKSGRSFLKG
          . . . . .

```

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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Search Result: eco:b3823 -> GENES

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cvi:CV GLYALAAAGLAMVMAHPLLFKIISSLGAAVLVWLVQGLRAASRPARAASGETAAAAPTSAAWRAARTG  
60 70 80 90 100 110 120

eco:b3 LLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIYETLAWFTVVASLFALPQMRRGYQRLAKWID  
40 50 60 70 80 90 100

cvi:CV LAVSLSNPHLAVMFVALLSQFVTADMPASGQALLIATAMGLDFGWYALLTLLISHPSILSGLHRKSRWID  
130 140 150 160 170 180 190

eco:b3 GFAGALFAGFGIHLIISR  
110 120

cvi:CV GCGGALLMLLGLRILVY  
200

>>son:S00765 threonine efflux protein, putative (234 aa)  
initn: 184 initl: 184 opt: 180 Z-score: 243.7 bits: 51.5 E0: 6.7e-06  
Smith-Waterman score: 180: 26.316% identity (27.027% ungapped) in 114 aa overlap (9-119:115-228)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKS—GRSFLKGLLTNLA  
10 20 30 40

son:SO ASYLAWMGFGALKATIAFFRKPKRLKGEAEASSVATEAQANTGDSQTKAEKSLSPRQGFMTGLYTNLL  
80 90 100 110 120 130 140

eco:b3 NPKAIIYFGSVFSLFVGDNVGTARWGIFALIIYETLAWFTVVASLFALPQMRRGYQRLAKWIDGFAGAL  
50 60 70 80 90 100 110

son:SO NPKALVFFLTLSALITPSVTPATKVAALVLFVLSLWFGFLALMLSKAKVQQAQRIPTIDAVIGVI  
150 160 170 180 190 200 210

eco:b3 FAGFGIHLIISR  
120

son:SO FMSVALAIVSNLLLV  
220 230

>>cef:CE2245 putative threonine efflux protein (224 aa)  
initn: 222 initl: 177 opt: 179 Z-score: 242.6 bits: 51.2 E0: 7.7e-06  
Smith-Waterman score: 198: 28.462% identity (31.092% ungapped) in 130 aa overlap (1-119:85-214)

eco:b3 MGYQMLRGALKK—EAVSAPAPQ—VEL  
10 20

cef:CE TVWVTLTVGAATLLTTPDILGVILVGGGYLTWGYRMGRGAVRELLDARAFRNSATRPIDAVAAL  
50 60 70 80 90 100 110

eco:b3 AKSGRSFLKGLLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIYETLAWFTVVASLFALPQMR  
30 40 50 60 70 80 90

cef:CE GTPGQAYRQGMATNLSNPKVIMYFAAILAPLMPANPSLAVALTIIAIIIVQTNVVFIMCVIVSTERIRK  
120 130 140 150 160 170 180

eco:b3 GYQRLAKWIDGFAGALFAGFGIHLIISR  
100 110 120

cef:CE AVLRAQPVFDGVAAVVFIAGVLTLYEGASQLLLG  
190 200 210 220

>>ojp:ojp1236 unnamed protein product; similar to amino acid effl (211 aa)  
initn: 177 initl: 177 opt: 178 Z-score: 241.5 bits: 50.9 E0: 8.8e-06  
Smith-Waterman score: 178: 26.230% identity (27.350% ungapped) in 122 aa overlap (1-119:88-207)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSG—RSFLKG  
10 20 30

[http://www.genome.jp/tmp/get\\_linkdb\\_fasta.25159/result\\_genes.html](http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html)

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